Listing of Claims:

1. (Previously presented) A method for the detection of cytosine methylation in DNA comprising the steps of:

a) bringing the DNA to be investigated into contact with a cytidine deaminase,

whereby the cytidine deaminase deaminates cytidine and 5-methylcytidine at different rates,

b) investigating the partially deaminated DNA with respect to its sequence, and

c) concluding, from the presence or the proportion of deaminated positions, the methylation status of the DNA to be investigated in said positions.

2. (Previously presented) The method according to claim 1, wherein the enzyme AID (activation-induced cytidine deaminase) is used as the cytidine deaminase.

3. (Previously presented) The method according to claim 1, wherein the DNA to be investigated is present at least partially in single-stranded form.

4. (Previously presented) The method according to claim 1, further comprising hybridizing the DNA to be investigated with oligomers, whereby the hybrids are present in single-stranded form at the cytosine positions under investigation.

5. (Previously presented) The method according to claim 4, wherein the single-stranded regions are between 3 and 20 nucleotides long.

6. (Previously presented) The method according to claim 4, wherein the single-stranded regions are between 5 and 12 nucleotides long.

7. (Previously presented) The method according to claim 4, wherein the single-stranded region is 9 nucleotides long.

8. (Previously presented) The method according to claim 4, wherein the oligomers have a length of 20 to 150 nucleotides.

9. (Previously presented) The method according to claim 4, wherein the oligomers have a length of 35 to 60 nucleotides.

10. (Previously presented) The method according to claim 4, wherein the oligomers are present in a concentration of 1 pM to 1000 nM.

11. (Previously presented) The method according to claim 4, wherein the oligomers are present in a concentration of 1 nM to 100 nM.

12. (Previously presented) The method according to claim 1, further comprising amplifying the DNA to be investigated after the enzyme treatment.

13. (Previously presented) The method according to claim 12, wherein the amplifying step comprises conducting a polymerase reaction.

14. (Previously presented) The method according to claim 13, wherein the amplifying step comprises conducting a polymerase chain reaction.

15. (Previously presented) The method according to claim 14, wherein the polymerase chain reaction comprises using methylation-specific primers.

16. (Previously presented) The method according to claim 14, wherein the polymerase chain reaction comprises utilizing at least one methylation-specific blocker oligomer.

17. (Withdrawn) The method according to claim 12, further characterized in that a repeated enzymatic conversion with a cytidine deaminase is conducted after the amplification.

18. (Withdrawn) The method according to claim 12, further characterized in that the amplificates are analyzed by means of methods of length measurement, mass spectrometry or sequencing.

19. (Withdrawn) The method according to claim 12, further characterized in that the amplificates are analyzed by means of the primer extension method.

20. (Withdrawn) The method according to claim 12, further characterized in that the amplificates are analyzed by hybridization to oligomer arrays.

21. (Previously presented) The method according to claim 12, further comprising analyzing the amplificates with the use of real-time variants.

22. (Previously presented) The method according to claim 21, wherein the analyzing step comprises conducting a Taqman or a Lightcycler method.

23. (Withdrawn) The method according to claim 12, further characterized in that several fragments are simultaneously amplified by means of a multiplex reaction.

24. (Withdrawn) Use of a method according to claim 1 for the diagnosis of cancer diseases or other disorders associated with a change in the methylation status.

25. (Withdrawn) Use of a method according to claim 1 for predicting undesired drug interactions, for the differentiation of cell types and tissues or for the investigation of cell differentiation.

26. (Withdrawn) Use of cytidine deaminases, which convert cytidine and 5-methylcytidine at different rates, for methylation analysis.

27. (Withdrawn) Use of cytidine deaminases, which convert cytidine and 5-methylcytidine at different rates, for the diagnosis of cancer diseases or other disorders associated with a change in the methylation status.

28. (Withdrawn) Use of cytidine deaminases, which convert cytidine and 5-methylcytidine at different rates, for predicting undesired drug interactions, for the differentiation of cell types and tissues or for the investigation of cell differentiation.

29. (Withdrawn) Use according to claim 24, further characterized in that the cytidine deaminase involves activation-induced cytidine deaminase (AID), a biologically active fragment of AID or a modification thereof.

30. (Withdrawn) A kit, which comprises the AID enzyme, a biologically active fragment of AID or a modification thereof as well as oligomers and the buffers necessary for the deamination, as well as optionally also a polymerase, primers and probes for an amplification and detection.